SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bowman, Michael

(ii) TITLE OF INVENTION: SECRETED PROTEIN BA3.1 AND POLYNUCLEOTIDES ENCODING SAME

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sprunger, Suzanne A.
(B) REGISTRATION NUMBER: 41,323
(C) REFERENCE/DOCKET NUMBER: GI5295A

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 498-8284
(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGGCGGTAC GATTTGTTAG ACACAGGAGA TGATCTTGAC CCTGATATCA TTAATATCCT 60

TCCTGCTTCT CCAACTGGTT CTCCTGTACA TTCTCCAGGA TCTCATTACC CCCATGGAGG 120

TGATGCGGGC AAGGGTCAGA GTACTGATCG GCTACTATCA ACAGAACCTC ATGAGGAAGT 180

ACCTAATATT CTTCAGCAAC CATTGGCCCT TGGTTACTTT GTATCAACTG CCAAAGCAGG 240

TCCATTACCT GACTGGTTCT GGTCAGCATG TCCTCAAGCA CAATATCAGT GTCCCCTTTT 300

TTCTTAAGGC CTCTTTGCAC CTCCACGTGC CTTCAGTGCA ATCTGACGAG CTGCTTCACA 360

GTAAACACTC CCACCCACTT GACTCAAATC AGACTTCAGA TGTCCTCAGG TTTGTTTTGG 420

AACAGTACAA TGCACTCTCC TGGCTAACCT GTGACCCTGC AACCCAGGAC AGACGCTCAT 480

GTCTCCCAAT TCATTTTGTG GTGCTGAATC AGTTATATAA CTTTATTATG AATATGCTGT 540

GATCTTCATT TGATGGAACT GTGCAAGAAA AGAACAAGGA AAAATGGATG TTTCGCTGCA 600

GGATTAAGTT ACAATTATCT TCTCAGTGAA GGTCATTTGT GATGGGGTCT AATTCTTATT 660

ACTTCAACAA ATATTGTTTT GACTTGGGGG GAGGGGCTAT AACCCTGCTA TTTTTCATTG 720

ACTCTATTGA ACTCTTTAGG ATGATGACTG ATCATACAAA ACGTATTATA ACATTTTCGT 780

AGCAAAATTA ACCTTTTTTT TTTCCAGTCA CAGTATTTGT GAAAAGTAAT GAGCCATAGT 840

ACCCAGTCAT GTTAAATGAA TATTAAAAGC ATGGAGAGGA AACATGAGGA ACAATGAATT 900

TCAACATATG GCTTCAGAAC ATGAAGATGT TCTTGTATGG ATTATAGTAT CTAGTATTCA 960

AAAATGCCTG CATCTCTTCT CTTATTTATT GTAAGTTTTT AAATGTATAA ATTGTCTTAT 1020

ATTTCTTAAC CTCTTTTATA AAAATTTTCC TAGAAGGTTT ATACTGCCAA AAAAAAAAAA 1080

AAAAAA 1086

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ile Leu Thr Leu Ile Ser Leu Ile Ser Phe Leu Leu Leu Gln Leu
1               5                  10                  15

Val Leu Leu Tyr Ile Leu Gln Asp Leu Ile Thr Pro Met Glu Val Met
            20                  25                  30

Arg Ala Arg Val Arg Val Leu Ile Gly Tyr Tyr Gln Gln Asn Leu Met
        35                  40                  45

Arg Lys Tyr Leu Ile Phe Phe Ser Asn His Trp Pro Leu Val Thr Leu
    50                  55                  60

Tyr Gln Leu Pro Lys Gln Val His Tyr Leu Thr Gly Ser Gly Gln His
65                  70                  75                  80

Val Leu Lys His Asn Ile Ser Val Pro Phe Phe Leu Lys Ala Ser Leu
                85                  90                  95

His Leu His Val Pro Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys
            100                 105                 110

His Ser His Pro Leu Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe
        115                 120                 125

Val Leu Glu Gln Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala
    130                 135                 140

Thr Gln Asp Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu Asn
145                 150                 155                 160

Gln Leu Tyr Asn Phe Ile Met Asn Met Leu
                165                 170
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